

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 25, 2003, 11:49:10 ; Search time 18.88 seconds

(Without alignments)
81.470 Million cell updates/sec

Title: US-09-869-540a-2_COPY_4_19

Perfect score: 95

Sequence: 1 MLRCMLGRVRCPCMOV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	56	2	S68499 melanin-concentrat
2	95	100.0	165	2	A36237 melanin-concentrat
3	95	100.0	165	2	I52634 melanin-concentrat
4	82	86.3	132	1	MTONIK melanin-concentrat
5	82	86.3	132	1	MTONIK melanin-concentrat
6	82	86.3	132	1	B32910 melanin-concentrat
7	82	86.3	132	2	S34653 melanin-concentrat
8	82	86.3	132	2	S34654 melanin-concentrat
9	82	86.3	132	2	A32910 melanin-concentrat
10	44.5	45.3	186	2	D91252 hypothetrical prote
11	43	45.3	3206	1	GNVSPV genome polypeptid
12	42	44.2	250	1	GT0968 probable methyltra
13	42	44.2	577	1	VBBE61 glycoprotein E - s
14	42	44.2	660	2	T27794 hypothetrical prote
15	42	44.2	1177	2	A63009 polyketide synthet
16	42	44.2	1489	2	G98274 hypothetrical prote
17	41	43.2	315	2	S03416 probable transposa
18	40.5	42.6	426	2	G02277 creatine transport
19	40.5	42.6	635	2	S23431 choline transport
20	40.5	42.6	635	2	A46061 Na(+)-dependent cr
21	40.5	42.6	635	2	JC2386 creatine transport
22	40.5	42.6	635	2	G20295 creatine transport
23	40	42.1	61	2	G34429 ATPase inhibitor 3
24	40	42.1	143	2	I47202 Ig heavy chain var
25	40	42.1	367	2	F69816 reticuline oxidase
26	40	42.1	368	2	AB2215 hypothetrical prote
27	40	42.1	567	2	F87594 conserved hypothet
28	40	42.1	1131	2	T19442 hypothetrical prote
29	40	42.1	1711	1	A55148 protein-tyrosine-p

30	39	41.1	111	2	S25343	ORIS protein - yea
31	39	41.1	170	2	A60630	4-hydroxyphenylace
32	39	41.1	173	1	CYCAG2	gamma-crystallin m
33	39	41.1	229	2	G86924	hypothetrical prote
34	39	41.1	404	2	H87635	Risake 2Fe-2S fam1
35	39	41.1	430	2	T47014	hypothetrical prote
36	39	41.1	430	2	AC0237	probable membrane
37	39	41.1	478	2	T27714	hypothetrical prote
38	39	41.1	519	2	D82522	type I restriction
39	39	41.1	535	2	T17212	hypothetrical prote
40	39	41.1	1286	2	T33476	hypothetrical prote
41	39	41.1	1583	2	F86366	protein F2624.8 l
42	39	41.1	1657	2	T15838	hypothetrical prote
43	39	41.1	4302	2	A38971	polycystic kidney
44	38.5	40.5	189	1	IYHU16	interferon alpha-I
45	38.5	40.5	189	2	I37584	IFN-alpha-N-protein

ALIGNMENTS

RESULT 1

S68499 melanin-concentrating hormone - mouse (fragment)

C.Species: Mus musculus (house mouse)

C.Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999

C.Accession: S68499 R.Qn: D.; Luddvig, D. S.; Gammeltoft, S.; Piper, M.; Pelleymounter, M. A.; Cullen, M. J.;

Nature 380, 243-246, 1996 A>Title: A role for melanin-concentrating hormone in the central regulation of feedin

A:Reference number: S68499; MUID:96207751; PMID:8637571

A:Accession: S68499

A:Molecule type: mRNA

A:Residues: 1-56 <OUD>

A:Experimental source: tissue hypothalamus

C:Keywords: hormone; hypothalamus; neuropeptide

F:119/Product: neuropeptide N-GE (fragment) #status predicted <NCE>

F:38-56/Product: melanin-concentrating hormone #status predicted <MAT>

Query Match 100.0%; Score 95; DB 2; Length 56;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MLRCMLGRVRCPCMOV 16

41 MLRCMLGRVRCPCMOV 56

RESULT 2

A36237 melanin-concentrating hormone precursor - rat

C.Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 16-Jul-1999

C.Accession: A36237; A37407; A37406

R:Thompson, R. C.; Watson, S. J.

DNA Cell Biol. 9, 637-645, 1990

A>Title: Nucleotide sequence and tissue-specific expression of the rat melanin concn

A:Reference number: A36237; MUID:91083836; PMID:2261081

A:Accession: A36237

A:Molecule type: DNA

A:Residues: 1-165 <RHO>

A:Cross-references: GB:M62641; MID:9205329; PIRN:AAA1581.1; PID:9205330

R:Nahon, J. L.; Presse, F.; Bittencourt, J. C.; Sawchenko, P. E.; Vale, W.

Endocrinology 125, 2056-2065, 1989

A>Title: The rat melanin-concentrating hormone messenger ribonucleic acid encodes mul

A:Reference number: A37407; MUID:90005146; PMID:2477226

A:Accession: A37407

A:Molecule type: mRNA

A:Residues: 1-165 <NAH>

A:Cross-references: GB:M29712; NID:9205327; PIDN:AAA1580.1; PID:9205328
R:Vaughan, J.M.; Fischer, W.H.; Hoeger, C.; Rivier, J.; Vale, W.
Endocrinology 125, 1660-1665, 1989
A:Title: Characterization of melanin-concentrating hormone from rat hypothalamus.
A:Reference number: A37406; MUID:89338286; PMID:2759038
A:Accession: A37406
A:Status: preliminary
A:Molecule type: protein
A:Residues: 147-165 <VAM>
C:Superfamily: melanin-concentrating hormone

Query Match 100.0%; Score 95; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 2; e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRCMGLGRVYRPMQOV 16
|||||

DB 150 MRCMGLGRVYRPMQOV 165

RESULT 3
152634
melanin-concentrating hormone precursor - human
N:Alternate names: prepro-melanin-concentrating hormone
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision-02-Jul-1996 #text_change 16-Jul-1999
C:Accession: 152634; 155414; A34551
R:Breton, C.; Schorpp, M.; Nahon, J.L.
Brain Res. Mol. Brain Res. 18, 297-310, 1993
A:Title: Isolation and characterization of the human melanin-concentrating hormone gene
A:Reference number: 152634; MUID:93316802; PMID:8336825
A:Accession: 152634
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 88-96; 'S', 98-100; 'V', 102-108; 'E', 110-121; 'D', 123-131; 'T', 133-142; 'V', 144-149
A:Cross-references: GB:S64288; NID:9402797; PIDN:AA827494.1; PID:9402798
R:Presepe, F.; Nahon, J.L.; Fischer, W.H.; Vale, W.
Mol. Endocrinol. 4, 632-637, 1990
A:Title: Structure of the human melanin concentrating hormone mRNA.
A:Reference number: A34551; MUID:91125371; PMID:2149166
A:Accession: A34551
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-41; 'F', 43-103; 'G', 105; 'Q', 107-112; 'D', 114-165 <PRE>
A:Cross-references: GB:M57703; NID:9187445; PIDN:AAA63214.1; PID:9187446
C:Genetics:
A:Gene: GDB:PMCH
A:Cross-references: GDB:128784; OMIM:176795
A:Map position: 12q23-12q24
A:Introns: 83/3; 150/1
C:Superfamily: melanin-concentrating hormone
C:Keywords: hormone; hypothalamus
F:1-21/Domain: signal sequence #status predicted <SIG>

Query Match 100.0%; Score 95; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 2; e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRCMGLGRVYRPMQOV 16
|||||

DB 150 MRCMGLGRVYRPMQOV 165

RESULT 4
MTON2K
melanin-concentrating hormone 1 precursor - chum salmon
N:Alternate names: MCH1
A:Reference number: MCH1
C:Species: Oncorhynchus keta (chum salmon)

C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 24-Nov-1999
C:Accession: JS0282; JS0048; A01472
R:Takayama, Y.; Wada, C.; Kawachi, H.; Ono, M.
Gene 80, 65-73, 1989
A:Title: Structures of two genes coding for melanin-concentrating hormone of chum sal
A:Reference number: A91618; MUID:90006787; PMID:2792771
A:Accession: JS0282
A:Molecule type: DNA
A:Residues: 1-132 <TRK>
A:Cross-references: GB:M27872; NID:9213452; PIDN:AAA9418.1; PID:9213453
R:Ono, M.; Wada, C.; Oikawa, I.; Kawazoe, I.; Kawachi, H.
Gene 71, 433-438, 1988
A:Title: Structures of two kinds of mRNA encoding the chum salmon melanin-concentrat
A:Reference number: A91598; MUID:89138019; PMID:2465207
A:Accession: JS0048
A:Molecule type: mRNA
A:Residues: 1-3; 'S', 5-132 <ONO>
A:Cross-references: GB:M23573; NID:9213456; PIDN:AAA9420.1; PID:9213457
R:Kawachi, H.; Kawazoe, I.; Tsudokawa, M.; Kishida, M.; Baker, B.I.
Nature 305, 321-323, 1983
A:Title: Characterization of melanin-concentrating hormone in chum salmon pituitaries
A:Reference number: A93316; MUID:84014069; PMID:6621686
A:Accession: A01472
A:Molecule type: protein
A:Residues: 116-132 <KAW>
C:Comment: For melanin-concentrating hormone 2, see PIR:MTON2K.
C:Comment: This hormone, isolated from the pituitary gland, has an activity antagonis
C:Genetics:
A:Gene: MCH1
C:Superfamily: melanin-concentrating hormone
C:Keywords: hormone; hypothalamus; pituitary
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-115/Domain: propeptide #status predicted <PRO>
F:116-132/Product: melanin-concentrating hormone #status experimental <MAT>
F:120-129/Disulfide bonds: #status experimental

Query Match 86.3%; Score 82; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 3e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRQMLGRVYRPMQOV 16
|||||

DB 118 MRCMGLGRVYRPMQOV 132

RESULT 5
MTON2K
melanin-concentrating hormone 2 precursor - chum salmon
N:Alternate names: MCH2
C:Species: Oncorhynchus keta (chum salmon)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 24-Nov-1999
C:Accession: JS0283; S04087; JS0049; B01472; A01472
R:Takayama, Y.; Wada, C.; Kawachi, H.; Ono, M.
Gene 80, 65-73, 1989
A:Title: Structures of two genes coding for melanin-concentrating hormone of chum sal
A:Reference number: A91618; MUID:90006787; PMID:2792771
A:Accession: JS0283
A:Molecule type: DNA
A:Residues: 1-132 <TRK>
A:Cross-references: GB:M27871; NID:9213454; PIDN:AAA9419.1; PID:9213455
R:Nahon, J.L.; Schoepfer, R.; Vale, W.
Nucleic Acids Res. 17, 3598, 1989
A:Title: cDNA sequence of salmon melanin-concentrating hormone exhibits similarities
A:Reference number: S04087; MUID:89263809; PMID:2471156
A:Accession: S04087
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-106; 'SP', 109-132 <NAH>
A:Cross-references: EMBL:X13685; NID:964142; PIDN:CAA31978.1; PID:964143
R:Ono, M.; Wada, C.; Oikawa, I.; Kawazoe, I.; Kawachi, H.
Gene 71, 433-438, 1988
A:Title: Structures of two kinds of mRNA encoding the chum salmon melanin-concentrat
A:Reference number: A91598; MUID:89138019; PMID:2465207

A:Accession: J50049
A:Molecule type: mRNA
A:Residues: 1-107, P, 109-132 <CON>
A:Cross-references: GB:M2574; NID:g213458; PIDN:AAA9421.1; PID:g213459
R:Kawanishi, H.; Kawazoe, I.; Tsubokawa, M.; Kishida, M.; Baker, B.I.
Nature 305, 321-323, 1983
A:Title: Characterization of melanin-concentrating hormone in chum salmon pituitaries.
A:Reference number: A93316; MUID:84014069; PMID:6621686
A:Accession: B01472
A:Molecule type: protein
A:Residues: 116-132 <KAN>
C:Comment: For melanin-concentrating hormone 1, see PIR:MONTK.
C:Comment: This hormone, isolated from the pituitary gland, has an activity antagonistic
C:Genetics:
A:Gene: MCH2
C:Superfamily: melanin-concentrating hormone
C:Keywords: glycoprotein; hormone; hypothalamus; pituitary
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-115/Domain: propeptide #status predicted <PRO>
F:116-132/Product: melanin-concentrating hormone #status experimental <MAT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:120-129/Disulfide bonds: #status experimental

Query Match 86.3%; Score 82; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 3e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRRCMOV 16
DB 118 MRCWGRVYRRCMEV 132

RESULT 6
B32910
melanin-concentrating hormone 2 precursor - chinook salmon
C:Species: Oncorhynchus tshawytscha (chinook salmon)
C>Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 16-Jul-1999
C:Accession: B32910
R:Manth, C.D.; Qiu, H.; Akil, H.; Watson, S.J.; Dixon, J.E.
Proc. Natl. Acad. Sci. U.S.A. 86, 4292-4296, 1989
A:Title: Two precursors of melanin-concentrating hormone: DNA sequence analysis and
A:Reference number: A32910; MUID:89264605; PMID:2471200
A:Accession: B32910
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <MIN>
A:Cross-references: GB:M2575; GB:J04562; NID:g213462; PIDN:AAA9423.1; PID:g213463
C:Superfamily: melanin-concentrating hormone

Query Match 86.3%; Score 82; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 3e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRRCMOV 16
DB 118 MRCWGRVYRRCMEV 132

RESULT 7
S34653
melanin-concentrating hormone 1 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S34653
R:Hall, L.
Submitted to the EMBL Data Library, July 1993
A:Reference number: S34653
A:Accession: S34653
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <HAL>
A:Cross-references: EMBL:X73837; NID:g935051; PIDN:CAA52059.1; PID:g935052
C:Superfamily: melanin-concentrating hormone

Query Match 86.3%; Score 82; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 3e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRRCMOV 16
DB 118 MRCWGRVYRRCMEV 132

RESULT 8
S34654
melanin-concentrating hormone 2 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S34654
R:Hall, L.
Submitted to the EMBL Data Library, July 1993
A:Reference number: S34654
A:Accession: S34654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <HAL>
A:Cross-references: EMBL:X73838; NID:g935053; PIDN:CAA52060.1; PID:g935054
C:Superfamily: melanin-concentrating hormone

Query Match 86.3%; Score 82; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 3e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRRCMOV 16
DB 118 MRCWGRVYRRCMEV 132

RESULT 9
A32910
melanin-concentrating hormone 1 precursor - chinook salmon
C:Species: Oncorhynchus tshawytscha (chinook salmon)
C>Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 16-Jul-1999
C:Accession: A32910
R:Manth, C.D.; Qiu, H.; Akil, H.; Watson, S.J.; Dixon, J.E.
Proc. Natl. Acad. Sci. U.S.A. 86, 4292-4296, 1989
A:Title: Two precursors of melanin-concentrating hormone: DNA sequence analysis and
A:Reference number: A32910; MUID:89264605; PMID:2471200
A:Accession: A32910
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <MIN>
A:Cross-references: GB:M25754; GB:J04561; NID:g213460; PIDN:AAA9422.1; PID:g213461
C:Superfamily: melanin-concentrating hormone

Query Match 86.3%; Score 82; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 3e-06;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 LRCMLGRVYRRCMOV 16
DB 118 MRCWGRVYRRCMEV 132

RESULT 10
D91252
hypothetical protein ECs4988 [imported] - Escherichia coli (strain O157:H7, substrati
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: D91252
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hon, C.
gasekara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91252

A:Status: preliminary
A:Molecule type: DNA
A:ReadId: 1-186 <HAV>
A:Cross-references: GS:BA000007: PTD:G13364466; GSPDB:GN0015
A:Experimental source: strain O157:H7, substrain RMD 0509952
A:Genetics:
A:Gene: ECs498

Query Match	46.8%	Score 44.5;	DB 2;	Length 186;
Best Local Similarity	57.1%	Pred. No. 5.9;		
Matches	8;	Conservative	2;	Mismatches 3;
				Indels 1;
				Gaps 1
Oy	2	LRCMGYRYRCMO	15	
Db	159	LECILNRKYRMO	171	

RESULT 11
 GMSVSP
 genome polyprotein - pea seed-borne mosaic virus (strain DPM)
 N:Contains: 47K protein; 49K proteinase (EC 3.4.22.-), nuclear inclusion protein a; 6K F
 A:polymerase (EC 2.7.7.48), nuclear inclusion protein b
 C:Species: pea seed-borne mosaic virus, PSBMV
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001
 C:Accession: J01331
 R:Johansen, E.; Raemussen, O.F.; Heide, M.; Borthardt, B.
 J. Gen. Virol. 72, 2625-2632, 1991
 A:Title: The complete nucleotide sequence of pea seed-borne mosaic virus RNA.
 A:Reference number: J01331; MDID:92044431; PMID:1940858
 A:Accession: J01331
 A:Molecule type: genomic RNA

A:	Cross-References:	68:D10930; 68:D01132; NID:g220995; P1DN:BAAL176.1; PID:g26190
C:	Comment:	Helper component-proteinase is required for aphid transmission and also has f
C:	Comment:	Cytoplasmic inclusion protein b has helicase activity.
C:	Comment:	Nuclear inclusion protein a is covalently linked to the genomic RNA and also
C:	Comment:	Nuclear inclusion protein b has RNA polymerase activity.
C:	Superfamily:	tobacco etch virus genome polyprotein
F:	Keywords:	ATP; coat protein; cysteine proteinase; genome-linked protein; hydrolase; i
F:	I.856/Product:	helper component-proteinase #status predicted <NTE>
F:	I.857-I.266/Product:	47k protein #status predicted <L7>
F:	I.267-I.900/Product:	cytoplasmic inclusion protein #status predicted <CTY>
F:	I.1351-I.1359/Region:	nucleotide-binding motif A (P-loop)
F:	I.1356-I.1443/Region:	nucleotide-binding motif B
F:	I.1440-I.1443/Region:	DExH motif
F:	I.1503-I.1953/Product:	6kR protein #status predicted <GRP>
F:	I.1956-I.2395/Product:	nuclear inclusion protein a #status predicted <NTA>
F:	I.2396-I.2915/Product:	nuclear inclusion protein b #status predicted <NTB>
F:	I.2916-I.3206/Product:	coat protein #status predicted <COA>
F:	I.2016/Binding site:	phosphoryl-RNA (Tyr) (covalent) #status predicted
Oy	Query Match	45.3%; Score 43; DB 1; Length 3206;
	Best Local Similarity	37.5%; Pred. No. 1.4e+02;
DB	Matches	6; Conservative
	Mismatches	5; Indels
	Gaps	0;
	1 MLCMLGRTVRCQMOY 16	
	: : : : : : : : : : :	
	436 ILAAOILRVFPCWRI 451	

RESULT 12
G70968
Probable methyltransferase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: G70968
R:Cole, S.T.; Brosch, R.; Parthail, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:Reference Number: A70500; M0ID:98293587; PMID:9634230

A:Accession: G70968
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-250 <COL>
A:Cross-references: GB:880225; GB:AL123456; NID:93242265; PIDN:CAB02328.1; PID:62664.4
A:Experimental source: strain H37Rv
C:Genetics:
C:Gene: RV2675c

Query Match	44.2%	Score 42	DB 2	Length 250
Best local Similarity	33.3%	Pred. No. 20		
Matches	9	Conservative	4	Mismatches
			2	Indels
			12	Gaps
1				
2	LRCL-----GAYRRPCMOY	16		
Db	218 VRCVLEFRRAIKFWLGVGGVHAPFMEV	244		

RESULT 13
VG8BGI
glycoprotein E - suid herpesvirus 1
C:Species: suid herpesvirus 1
A:Note: host Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #ext_change 16-Jul-1999
C:Accession: B29012
R:Protein(s): E.A.: Timmins, J.G.; Post, L.E.
J: J.Virol. 60, 185-193, 1986
A:Title: Use of lambda-tell to isolate genes for two pseudorabies virus glycoproteins
A:Reference number: A93021; M0ID:86508#35; PMID:3018284
A:Accession: B29012
A:Molecule type: DNA

```

QY      3 RCMGRTYRRC 13
DB      273 RCLLYTYEPC 283

A:Cross-references: GB:M14336; NID:9334035; PIDD:AAIC352405.1; PID:9333403;
C:Experimental source: strain Rice
C:Superfamily: herpesvirus glycoprotein E
C:Keywords: glycoprotein
F:87,93,185,258,343/Binding site: carbohydrate (Asn) (covalently) status predicted
Query Match      44.2%; Score 42; DB 1; Length 577;
Best Local Similarity 63.6%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

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RESULT 14
T22794
hypothetical protein F56H6.1 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C|Accession: T22794
R|Kershaw, J.
submitted to the EMBL Data Library, November 1996
A|Reference number: Z19617
A|Accession: T22794
A|Status: preliminary; translated from GB/EMBL/DDBT
A|Molecule type: DNA
A|Residues: 1-660 <MW>
A|Cross-references: EMBL:Z81553; PIDN:CAB04490.1; GSPDB:GN0019; CESP:F56H6.1
A|Experimental source: clone F56H6
C|Genetics:
A|Gene: CESP:F56H6.1
A|Map position: 1
A|Intons: 34/2; 54/2; 197/3; 283/3; 323/3; 384/1; 404/3; 452/2; 493/2; 538/2; 591/1
Query Match          44.2%; Score 42; DB 2; Length 660;
Best Local Similarity 33.3%; Pred. NO. 47;
Matches      5; Conservative      5; Mismatches      5; Indels      0; Gaps      0;
OY    2 LRCMIGRYRPCMOV 16
:::|:| | :

```

db 504 MRCVERIYNGLMNI 518

RESULT 15

AG3009

polyketide synthetase Atu3681 [imported] - Agrobacterium tumefaciens (strain C58, Dupont

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AG3009

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavln, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG3009

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-1477 <KUR>

A:Cross-References: GB:AE008689; PIDN:AAL4453.1; PID:917742100; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu3681

A:Map position: linear chromosome

Query Match

Best Local Similarity 44.28; Score 42; DB 2; Length 1477;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 RYRRCWQ 15

Db 894 RYRPTWQ 901

Search completed: June 25, 2003, 11:55:45
Job time : 19.88 secs